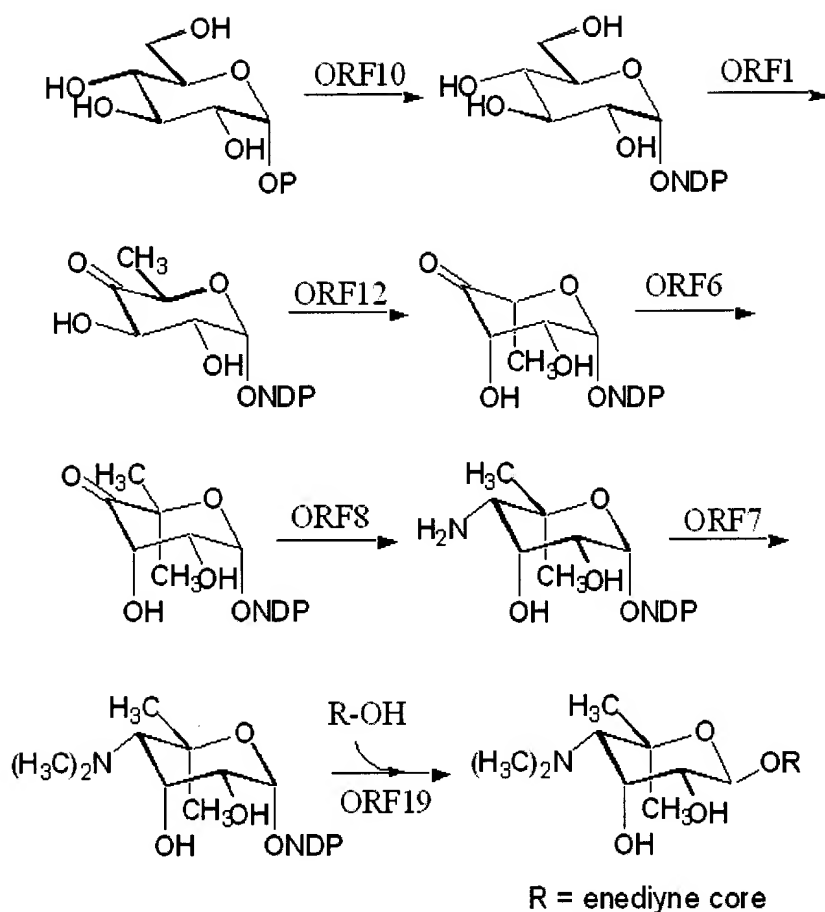


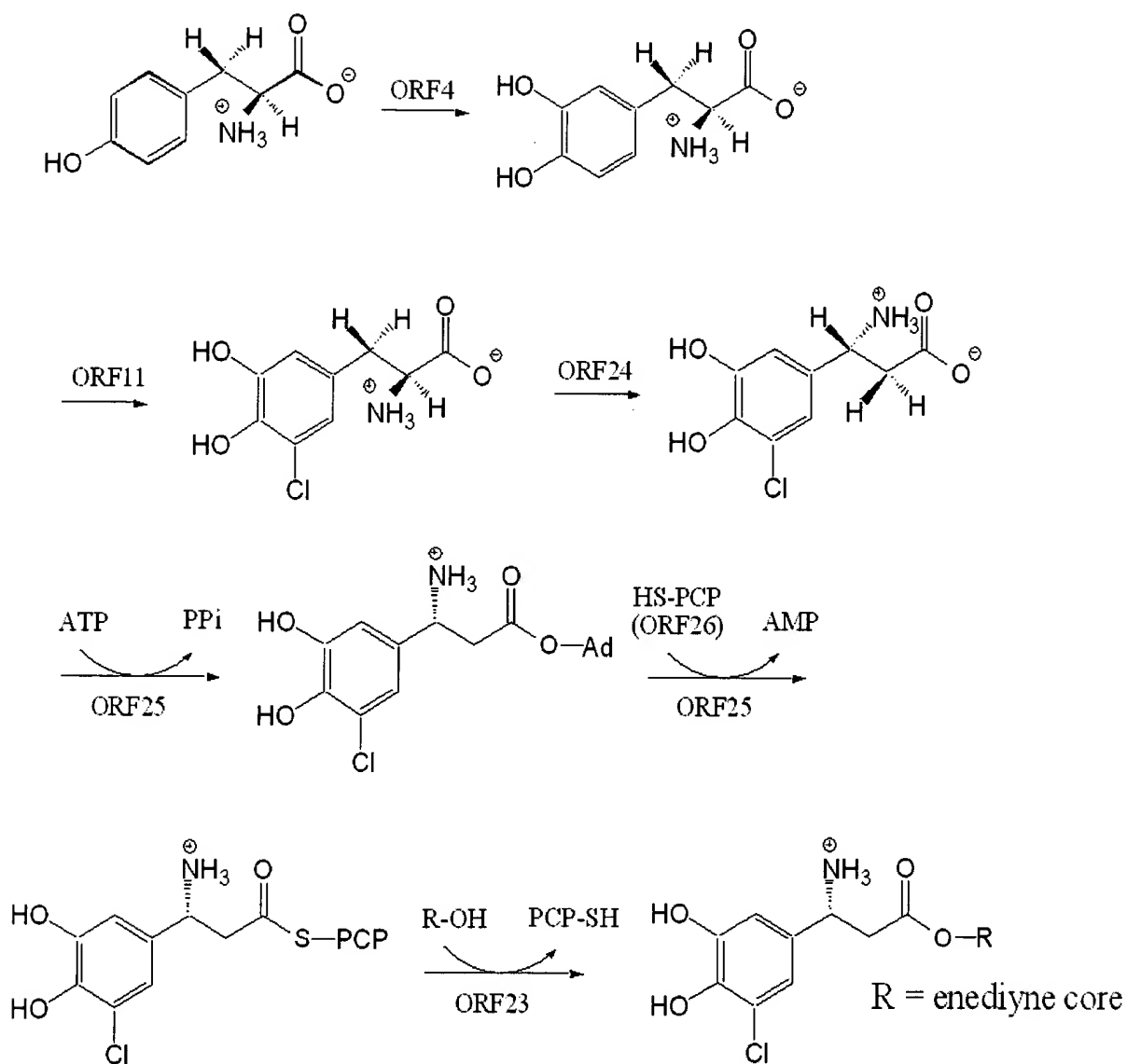
Fig. 1



ORF10: dNDP-glucose synthase, 355 aa
 ORF1: dNDP-glucose dehydratase, 332 aa
 ORF12: epimerase, 192 aa
 ORF8: aminotransferase, 410 aa

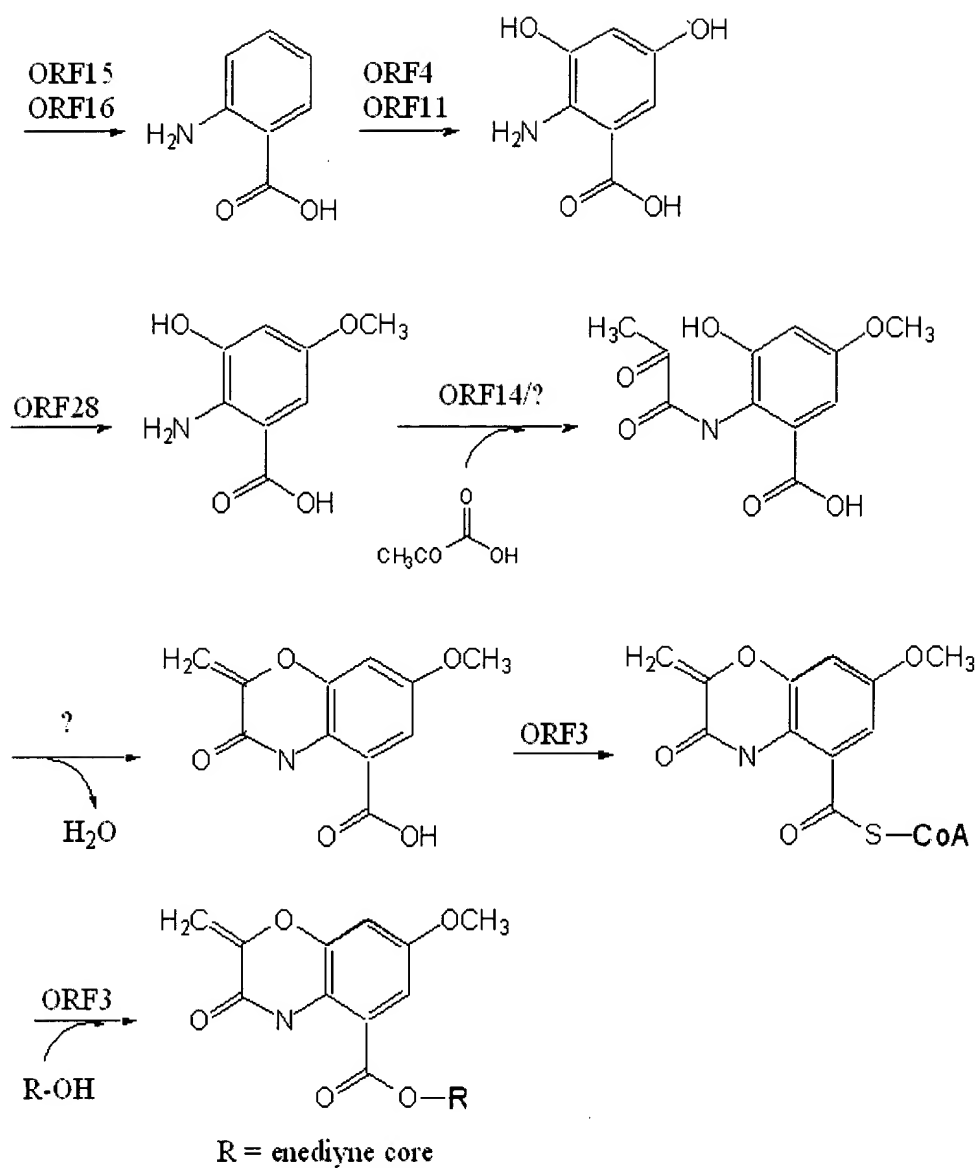
ORF6: C-methyltransferase, 423 aa
 ORF7: N-methyltransferase, 244 aa
 ORF19: glycosyl transferase, 459 aa

Fig. 2



- ORF4:** Hydroxylase, 527 aa
ORF11: Hydroxylase halogenase, 492/494 aa
ORF24: Aminomutase, 539 aa
ORF23: Type II NRPS condensation enzyme, 459 aa
ORF25: Type II NRPS adenylation enzyme, 716 aa
ORF26: Type II peptidyl carrier protein 93 aa

Fig. 3A



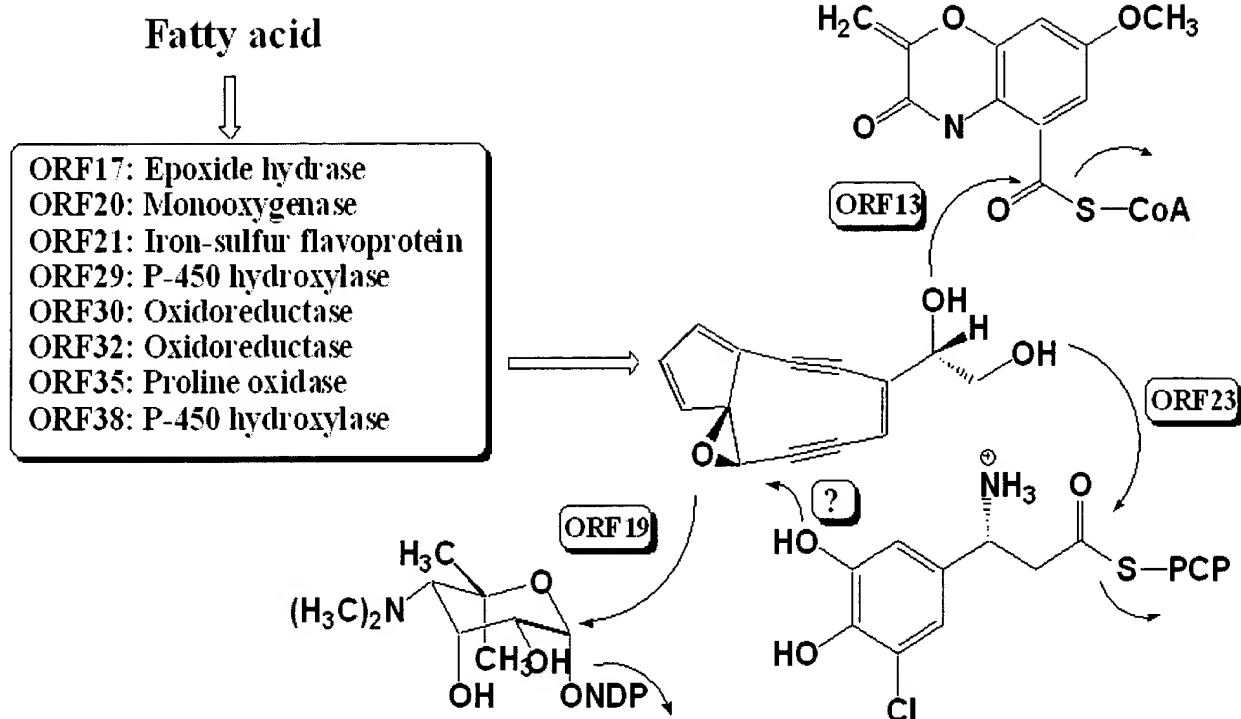
ORF15: Anthranilate synthase I, 493 aa
 ORF16: Anthranilate synthase II, 220 aa
 ORF28: O-methyltransferase, 350 aa

ORF3: Coenzyme F390 synthetase, 463 aa
 ORF14: Coenzyme F390 synthetase, 484 aa
 ORF13: O-acyltransferase, 378 aa

Fig. 3B

ORF15: Anthranilate synthase I, 493 aa

ORF16: Anthranilate synthase II, 220 aa



ORF13: O-acyltransferase,
 ORF19: Glycosyl transferase,
 ORF23: Type II NRPS condensation enzyme

Fig. 4

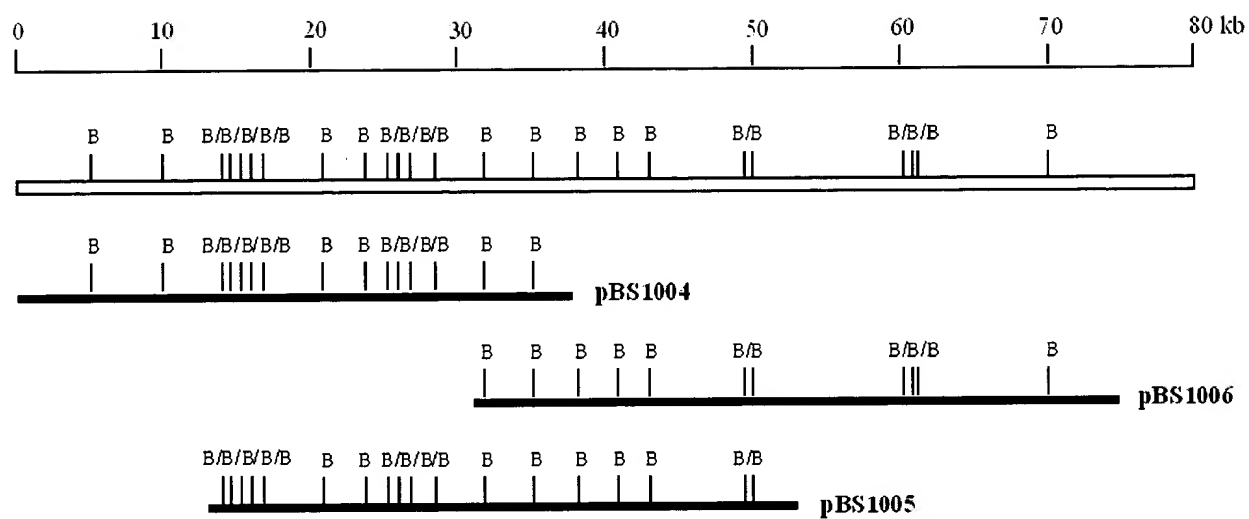


Fig. 5A

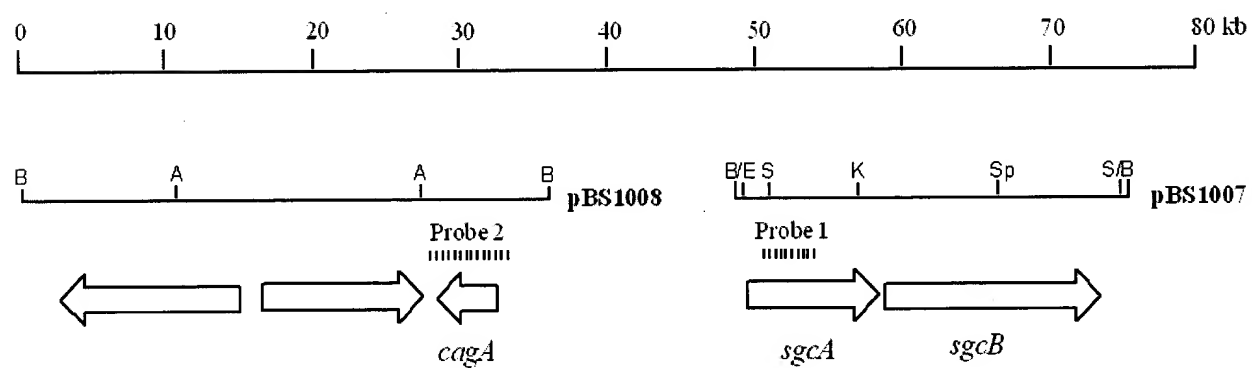


Fig. 5B

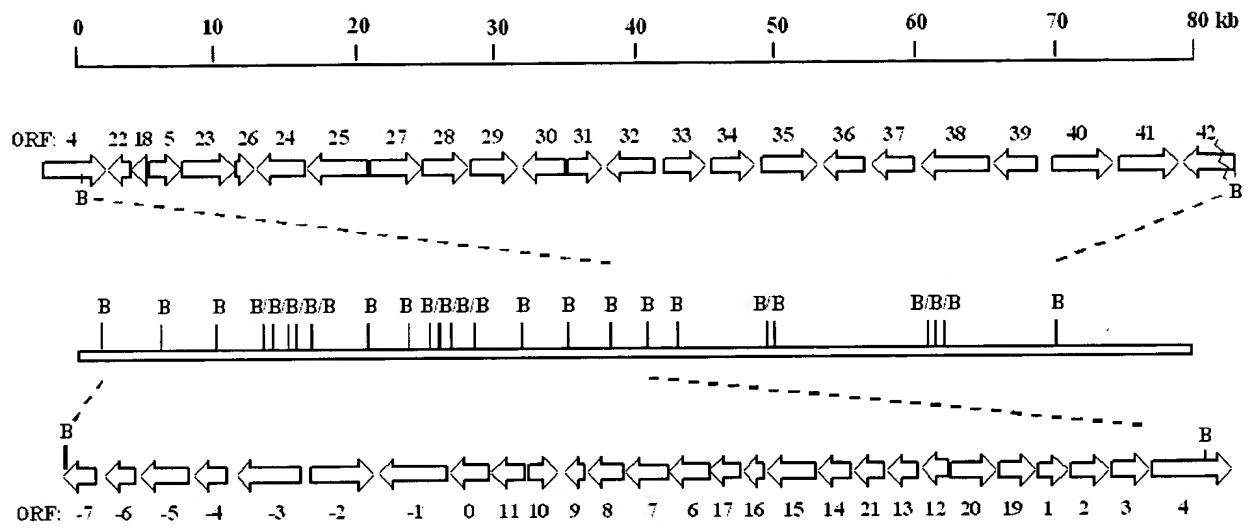


Fig. 5C



Gdh
TyLA2
SgcA
MtmE
consensus

1: ~MRVLVTGGAGFIGSHYVRQLLGGAYPAFAFAGADV VLDKLTAYAGNEENLRPVADDPRE: 57
1: ~MRVLVTGGAGFIGSHFTGQLLTGAYEDDLGATRTV VLDKLTAYAGNPANLEHVAGHPDL: 57
1: ~MRMLVTGGAGFIGSQFVRATLHGELEPGSEDARVT VLDKLTYSGNPANLTSVAAPRY: 57
1: MTTSILVTGGAGFIGSHYVRTLLGPR..GVPDVTVT VLDKLTAYAGTLTNLAEVSDSDRE: 58
1: mrvlvtggagfigshyvr ll g pa v vldkltYaGn NL Va prf: 60

Gdh
TyLA2
SgcA
MtmE
consensus

58: RFVRGDI CEWDV VSEVVMREV DVVVFHAAET FHVDRSIL GASDE VVTVNVVGTNTLLIQGALAA: 117
58: EFVRGDIADHGWRRLMEGVGLVVFHAAESHVDRSIESSEAFVRTNVEGTRVLLQAAVDA: 117
58: TEVQGDIVDPVRVDEVVAGHDVIVVFHAAESHVDRSIDTATRFTTNVLGTQTLLEAALRH: 117
59: RFVRGDI CDAPLVDLLAVHDQVVFHAAESHVDRSILGADEVR TNVTGTQTLTD AALRQ: 118
61: FVRGDI d vv evm dvvVFHAAESHVDRSI a EV TNV GTntll aal : 120

Gdh
TyLA2
SgcA
MtmE
consensus

118: NVSKFVHVSTDEVYGTIEHGSWPEHDLEPNSPYSAAKAGSDLIARAYHRT HGLPVCITR: 177
118: GVGRFVHISTDEVYGSIAEGSWPEHDHVPAPNSPYAATKAASDILLALAYHRT YGLDVRVTR: 177
118: GVGRFVHVSTDEVYGSIAEGSWTEDTPLAPNPVYAAASKAGSDLMALAWHRT RGLDVVTR: 177
119: GLETFVHISTDEVYGSIDA GSWPETAEVSPNSLYSAAKASDDLVALAYHRT HGLDVRVTR: 178
121: gv kFVHVSTDEVYGSi GSWpEd pl PNsPy A KAgSDLiAlAYHRT hGLdV vTR: 180

Gdh
TyLA2
SgcA
MtmE
consensus

178: CSNNYGPYQFFPEKVLPLFTI TNLMGRRR VPLYGDGLNVRDWLHVTDHCRGLIQLVAES GRAG: 237
178: CSNNYGPYQYPEKAVPLFTI TNLLDGLP VPLYGDGNTREWLHVDDHCRGVALLV GAG GRP: 237
178: CTNNYGPYQYPEKVIPLFVTNILLDGLR VPLYGDGAHRRDWLHVSDHCRATQMMN SGRAG: 237
179: CSNNYGS HQFFPEKVIPLFVTISLLDGRE VPLYGDGTNVRDWLHVDDHVRAIE LVRTGGRAG: 238
181: CSNNYGP QfPEKVIPLFiTnllDG VPLYGDG n RdWLHV DHcRgi lV GRAG: 240

Gdh
TyLA2
SgcA
MtmE
consensus

238: EINYIGGGTELTNKELTERTVLELMGQDWSMVQPVTDRKGHDRRY SVDHHTKI SEELGYEPV: 297
238: VINYIGGGTELTNAELTDRI TELCGADRSALRRVADRP GHDRRY SVD TTKIR EELGYAPR: 297
238: EYHIGGGTELSNEELTGLLLTA CGTDWSCVDRVADROGHDRRYSLDITKIROELGYEPL: 297
239: EYNYIGGGTELSNKELTQLLLDACCAGWDRVRYVTDRKGHDRRY SVDCTKIRRELGYRPA: 298
241: eiYnIGGGTELTn ELT vle cg dws v V DR GHDRRY SVD TKIR ELGY P : 300

Gdh
TyLA2
SgcA
MtmE
consensus

298: VPERGLAETIEWYRDNRAWWEPLKSA PDGGK~~~: 329
298: TGITEGLACTVAWYRDNRAWWEPLKSPG GRELERA: 333
298: VATEDGLAATVKWYHENRSWQPLKEAAGLLDAVG~: 332
299: REFGDALAETVAWYRHHRAWWEPLTRAYCAVAA~~~: 331
301: f egLA lV WYrDnRawWePlk a gg : 336

Fig. 7

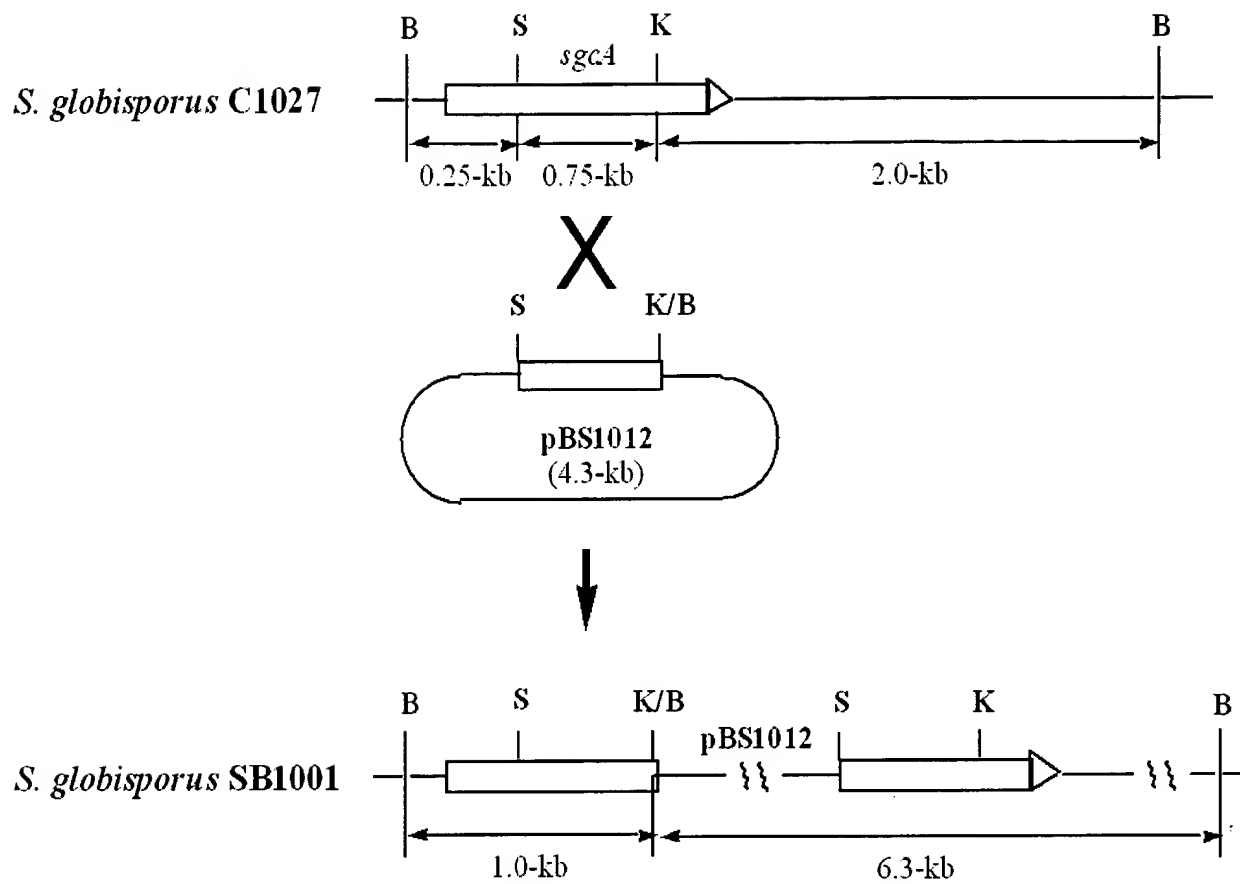


Fig. 8A

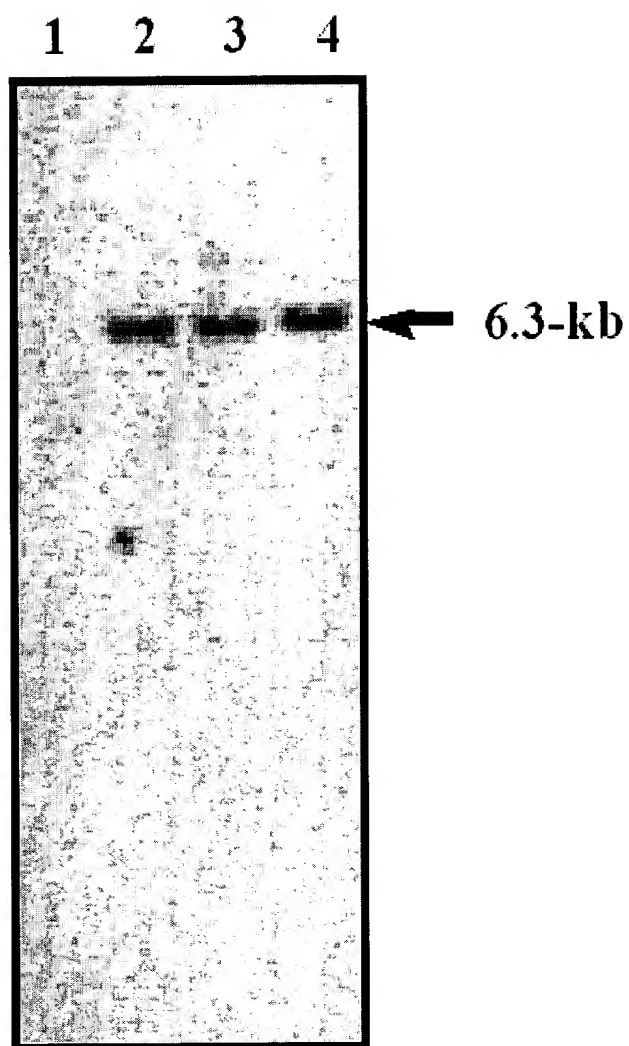


Fig. 8B

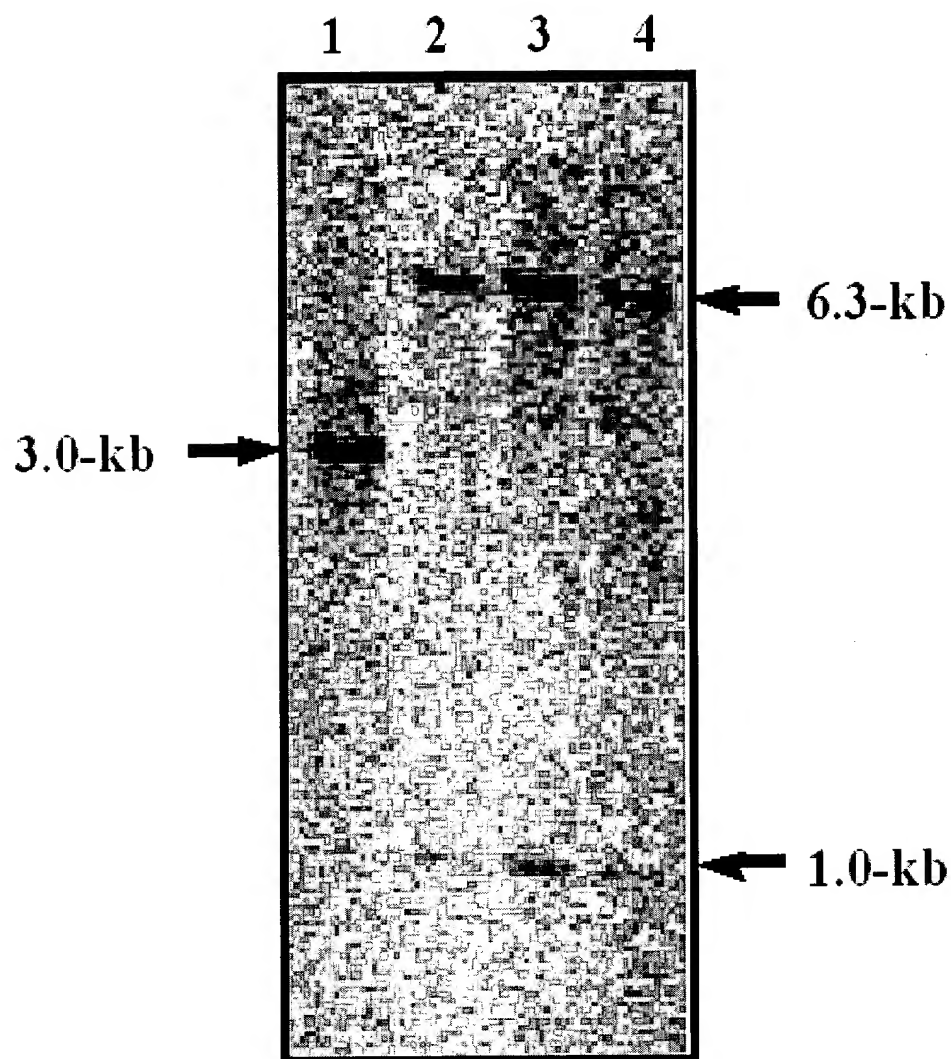


Fig. 8C

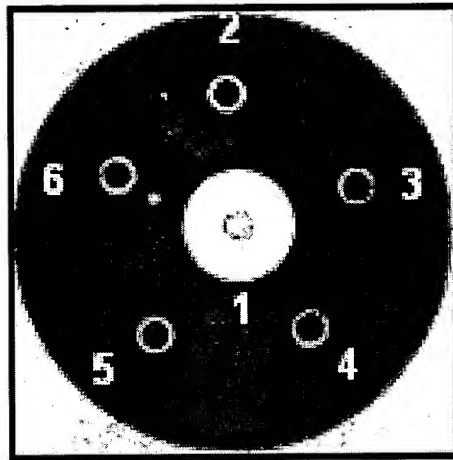


Fig. 9A

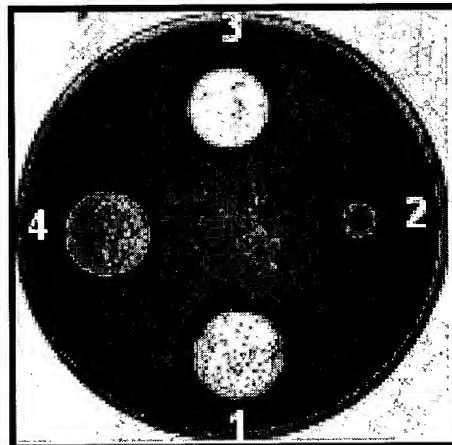


Fig. 9B

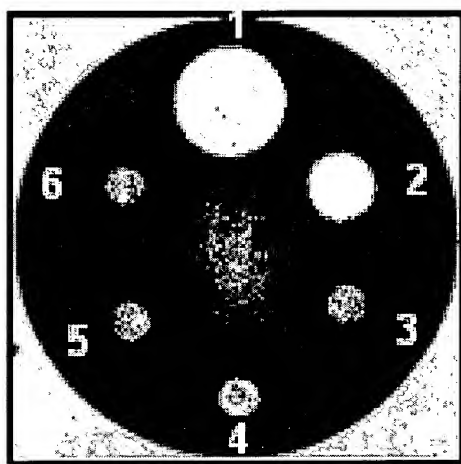


Fig. 9C

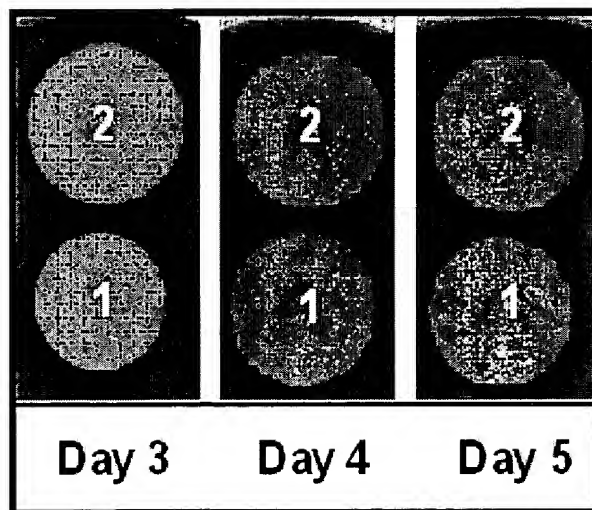


Fig. 9D

| | | | | | | | | |
|------|---|--------------|---------------|--|------|-------|---------------|------|
| 1 | GGATCCGGGAAGACCGGAATTCCGCCCCCAGCCCGGTCGAAC | BamHI | EcoRI | CTGTAATCGTCTCGGTAGAACTGACGAAGCGTCA | CGCC | GTGAC | AAGGAGCGGACCG | 100 |
| 101 | ATGAGGATGCTGGTGACGGGGCGGAGCGGGTTT | | | CATCGGGTCGCGAGTTCTGTCGGGGCCACACTGCACGGCGAGCTGCCGGGTCCGAGGACGCCCGGGTGA | | | sgcA > | 200 |
| | M R M L V T G G A G F I G S Q F V R A T L H G E L P G S E D A R V T | | | | | | | |
| 201 | CGGTCTTGACAAGCTGACGTACTCCGGCAATCCGGCAACCTCA | | | CCCTCCGCGGCCCATCCCGGTACACCTTCGTCCAGGGCGACACCGTCGACCC | | | | 300 |
| | V L D K L T Y S G N P A N L T S V A A H P R Y T F V Q G D T V D P | | | | | | | |
| 301 | CGCGTCGTCGACGAGGTGGTCGCCGGCCACGACGTCACTTC | | | GCGCGGAGTCGCACGTGGACCGCTCGATCGACACCGCCACCGGGTTCGTC | | | | 400 |
| | R V V D E V V A G H D V I V H F A A E S H V D R S I D T A T R F V | | | | | | | |
| 401 | ACGACCAAGTGTCTCGGAGCCACAGCGTGTGGAAGCGGCT | | | CTCCGGACGGGTTCGGTTCACGTGTGACCGACGAGGTCTACGGGTCGA | | | | 500 |
| | T T N V L G T Q T L L E A A L R H G V G R F V H V S T D E V Y G S I | | | | | | | |
| 501 | TCGCCTCCGGCTCATGGACCGAGGACACCCCGTCGCCCA | | | CGTCCCTACCGGGCTCGAAGCGGGTTCGGACCTGATGGCGCTCGCCTGGCACCG | | | | 600 |
| | A S G S W T E D T P L A P N V P Y A A S K A G S D L M A L A W H R | | | | | | | |
| 601 | CACCGGGGCTGGACGTCTGTCACCCGGTGCACCAACA | | | CTAGGTCCTACCAGTACCCCGAGAAGGTGATCCCCGTCTTCGTCAACCAATCCTC | | | | 700 |
| | T R G L D V V V T R C T N N Y G P Y Q Y P E K V I P L F V T N I L | | | | | | | |
| 701 | GACGGCTTGCGGTGCCCTGTACGGGACGGCGGCCAC | | | CGCGGACTGGCTGCACGTGCCGACCACTGCCGGGCCATCCAGATGGTCATGAACCTCCG | | | | 800 |
| | D G L R V P L Y G D G A H R R D W L H V S D H C R A I Q M V M N S G | | | | | | | |
| 801 | GCCGGCCGGGAGGTCTACCACATCGCGGGCGGCAC | | | CGAACTCTCAACGAGGAACCTACCGGCCCTGTGCTCACGGCGTGCGGCACCGACTGGTCCTG | | | | 900 |
| | R A G E V Y H I G G T E L S N E E L T G L L T A C G T D W S C | | | | | | | |
| 901 | CGTGACCGGGTGGCCGACGGGCACGACCCCGCTACT | | | CGCTCGACATCACGAAGATCCGGCAGGAACCTGGGTACGAGCCCCCTGGTCGCCTTC | | | | 1000 |
| | V D R V A D R Q G G H D R R Y S L D I T K I R Q E L G Y E P L V A F | | KpnI | | | | | |
| 1001 | GAGGACGGCCTGGCCCGACGGTGAAGTGGTATCACG | | | AGAACCTTCGTGGCAGCCCGCTGAAGGAAGCGGCCCGCCCTCCTGGACGCCCTCGGCTGAC | | | | 1100 |
| | E D G L A A A T V K W Y H E N R S W W Q P L K E A A G L L D A V G * | | | | | | | |
| 1101 | GGCAGCCACCGCTAGGAACACCCACG | | | GAAAG | | | | 1200 |
| | | | | GAGCACTCCGTCACAGCAGTCAAGGAGCCGACGTCCCGCAGGACGGCGGAGTGGATCGCTCTCG | | | | |
| 1201 | TCGTCTCTCTTGGCCACGATGCTGTTGATG | | sgcB > | M T A V K E P T S R A G R R E W I A L V | | | | 1300 |
| | V L S L P T M L L M L D I N V L M L A L P Q L S E D L G A S S T Q | | | | | | | |
| 1301 | ACAGTGTGGATCACCGACATCTACGGATTCCGGAT | | | CGCCGGCTTCTTGGTGACCATGGGCACCTTCGGCAGCCGATCGGCCCGCAGGCTCCTGCTC | | | | 1400 |
| | Q L W I T D I Y G F A I A G F L V T M G T L G D R I G R R L L L | | | | | | | |
| 1401 | GGGGCGGGCCGTCTTCGCGTCTGTCGCGCGTCTCC | | | GACAGCGCGCGATGCTCTGTCGTACGCCCGCCGTGCTCGGGCTCGCCGGG | | | | 1500 |
| | G G A A V F A V V S V V A A F S D S A A M L V V S R A V L G V A G A | | | | | | | |
| 1501 | CCACGGTGATGCCCTCGACGCTCGCGTCA | | | TACGCAACATGTTCCGAGGACCCCAAGGAGCGGGCACCCGCCATCGCCATGTGGCGAGCGCCATGATGGC | | | | 1600 |
| | T V M P S T L A L I S N M F E D P K E R G T A I A M W A S A M M A | | | | | | | |
| 1601 | CGGAGTCGCCCTCGGGCCCGCTCGCGCGTTC | | | TGGTGGGATCGGTGTTCTCATCGCCCGTTCCGGTGATGCTGCTGTTG | | | | 1700 |
| | G V A L G P A V G G L V L A A F W W G S V F L I A V P V M L L V V | | | | | | | |

Fig. 6



1701 GTCACGGCCCCGTGCTCACCAGTCCCGCAGACCCGGACGCCGGACGGCTGGACCTGCTAGCGCGGGGCTCTCCCTCGCGACCGTGTGCGCGTGA
V T G P V L L T E S R D P D A G R L D L L S A G L S L A T V L P V I 1800
1801 TCTACGGACTGAAGGAGTGGCCCCGAGACCGGGTGGGACCCGCTCGCGCGCGGTGGTCTCGCGCGTGTCTCGCGCGGTGCTGCTCCAGCGCCA
Y G L K E L A R T G W D P L A A G A V L G V I F G A L F V Q R Q 1900
1901 GCGGGGTTGGCCGACCCCATGCTGGACCTCGGCCCTCTTCGCCGACCCGACCCCTGCGGGCGGTCTGACGGTCACTGTGGTCAACGCCGTATCATGGGC
R R L A D P M L D L G L F A D R T L R A G L T V S L V N A V I M G 2000
2001 GGGACCGGACTGATGGTCCGCTGTACCTCCAGACGATCGCCGGTCACTCCCGCTTGGCCCGCGGGCTGTGGCTGCTGATCCCGGCCCTGCATGCTCGTCG
G T G L M V A L Y L Q T I A G H S P L A A G L W L I L I P A C M L V V 2100
2101 TGGGCGTACAGTGTGCAACCTGCTGGCCCCAGGGATGCCCTTCCCGGTGCTGTGGGGGACTGTGATCGCGCGTTCGGACAGCTCCTGATCAC
G V Q L S N L L A Q R M P P S R V L L G G L I A V G Q L L I T 2200
2201 CCAGGTGGACACCGAGGACACCGCCCTCCTCATCGCGGCCACCACTGATCTACTTCCGGCCCTCACCGTGGGGCCGATCACCGGGCGGATCATG
Q V D T E D T A L L I A A T T L I Y F G A S P V G P I T T G A I M 2300
2301 GGAGCCGCCCCCGGAGAGGCGGTGCCCTCGTCTGCTCCGCCACCGCGCGGAGTTTCGGAGTGGCGCTCGGCATCGCGGGCCCTGGGGAGTCTGG
G A A P P E K A G A S S L S A T G G E F G V A L G I A G L G S L G 2400
2401 GCACCGTCTGTACAGCGCCGGGTGAGGTGCCGACCGCGCGGCCCGACCGCGAGAGCATCGCGCGCCCTGCACACGGC
T V V Y S A G V E V P D A A G P A D A Q E S I A G A L H T A 2500
2501 CGGTACGCTGGCACCGGGCAGCGCGACGCCCTGCTGGACTCCGCGCGCGGCCCTTACAGCGCGTGCAGTCCGCGCGTCTGCGCGCTGTTTC
G Q L A P G S A D A L L D S A R A A F T S G V Q S V A A V C A V F 2600
2601 TCCCTGGCGCTCGCCGTCTCATCGGCACCCGGTCCGGGACATTTCCCGGATGGACCGGCGAGGAAACCGCGCGAGAACGACGCTCAACCGG
S L A L A V L I G T R L R D I S A M D H G H G E P A E N D A Q P A 2700
2701 CCACATGAGCGCACTTCCGGAGATGCAACGGCCCGCTCGAGGTATGAGGATCACCTTCCGGGGTGCACCTGCACGGCAACGGAGCGGTAGTGGAGTACT
T * 2800
2801 GGAACAGCAGCGGGAGACCATGCCCGCCGAGAACTCGAACAGTGGCAGGCTCCAGGCCGCCATGGACCAACGCGCAAGAGGCTTTTCGCCCTT
2900
2901 CTGGCGGGAACGACTCCCCCGAGAACATCACCTCCATGGCGGACTACGGCGCGGGTGCCTCTCTGCGCAAGGCCGACCTCTCTCGCGCGGAAAGCGCGG
3000
3001 TCTCCCCCTTACGGCACCTGGCCCCCTCGCTGGATCC 3035

Sphi

SacII

BamHI

Fig. 6 cont'd.

